

SEQUENCE LISTING

5 <110> Syngenta Biotechnology, Inc.
Grina, Jonas

<120> NOVEL CYANOENAMINES USEFUL AS LIGANDS FOR MODULATING GENE EXPRESSION
IN PLANTS OR ANIMALS

10 <130> 1392/2/2

<150> 60/272,905

15 <151> 2001-03-02

<160> 12

<170> PatentIn version 3.1

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cttcggattg tgttttgact gaaaagcgac gcgtatcgtg gtcgaagatt ctctataagt 180
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40 gttcatgccc gtagagacgc gtttagatag ttatggcgag gaaaaagtga agtgaaagcc 300
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atg aga cgc cgc tgg tca aac aac gga tgt ttc cct ctg cga atg ttt 408
Met Arg Arg Arg Trp Ser Asn Asn Gly Cys Phe Pro Leu Arg Met Phe
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gag gag agc tcc tct gaa gtg act tct tcc tcg gcg ttc ggg atg ccg 456
Glu Glu Ser Ser Ser Glu Val Thr Ser Ser Ser Ala Phe Gly Met Pro
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gcg gcc atg gta atg tca ccg gag tcg ctg gcg tcg cca gag tac ggc 504
Ala Ala Met Val Met Ser Pro Glu Ser Leu Ala Ser Pro Glu Tyr Gly
35 40 45
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15	atg cct cct aca act cct aaa tca gag aac gag tcc atg tcg tca ggt Met Pro Pro Thr Thr Pro Lys Ser Glu Asn Glu Ser Met Ser Ser Gly 100 105 110	696
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25	gaa ctg tgc ctt gtt tgc ggc gac agg gct tcg gga tat cac tat aac Glu Leu Cys Leu Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn 145 150 155 160	840
30	gcg ctt acg tgc gaa gga tgt aaa ggg ttc ttc agg cgg agt gtg acc Ala Leu Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr 165 170 175	888
35	aag aat gcg gta tat att tgt aaa ttt gga cac gcc tgc gag atg gac Lys Asn Ala Val Tyr Ile Cys Lys Phe Gly His Ala Cys Glu Met Asp 180 185 190	936
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5	ccg ctg tgc gcg aac cag aag tcc ctg atc gcg agg ctc gtg tgg tac Pro Leu Ser Ala Asn Gln Lys Ser Leu Ile Ala Arg Leu Val Trp Tyr 290 295 300	1272
10	cag gag ggg tac gag cag ccg tgc gag gaa gat ctc aag aga gtt aca Gln Glu Gly Tyr Glu Gln Pro Ser Glu Glu Asp Leu Lys Arg Val Thr 305 310 315 320	1320
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35	aac cag gcg tac acg cgc gac aac tac cgc aag gcg ggc atg tcc tac Asn Gln Ala Tyr Thr Arg Asp Asn Tyr Arg Lys Ala Gly Met Ser Tyr 405 410 415	1608
40	gtc atc gag gac ctg ctg cac ttc tgt cgg tgt atg tac tcc atg agc Val Ile Glu Asp Leu Leu His Phe Cys Arg Cys Met Tyr Ser Met Ser 420 425 430	1656
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45	gac cgg cca ggc ctc gag caa ccc ctt tta gtg gag gaa atc cag aga Asp Arg Pro Gly Leu Glu Gln Pro Leu Leu Val Glu Glu Ile Gln Arg 450 455 460	1752
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55	tgc cct cgc tgc gcc gtg ctg ttc ggc aag atc ctc ggc gtg ctg acg Ser Pro Arg Cys Ala Val Leu Phe Gly Lys Ile Leu Gly Val Leu Thr 485 490 495	1848

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Gly Glu Pro Arg Arg Gln Lys Lys Gly Pro Ala Pro Arg Gln Gln Glu
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Pro Leu Ser Ala Asn Gln Lys Ser Leu Ile Ala Arg Leu Val Trp Tyr
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 10 Glu Phe Ala Lys Gly Leu Pro Gly Phe Ser Lys Ile Ser Gln Ser Asp
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 Gln Ile Thr Leu Leu Lys Ala Ser Ser Ser Glu Val Met Met Leu Arg
 370 375 380
 15 Val Ala Arg Arg Tyr Asp Ala Ala Thr Asp Ser Val Leu Phe Ala Asn
 385 390 395 400
 Asn Gln Ala Tyr Thr Arg Asp Asn Tyr Arg Lys Ala Gly Met Ser Tyr
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 Met Asp Asn Val His Tyr Ala Leu Leu Thr Ala Ile Val Ile Phe Ser
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 Asp Arg Pro Gly Leu Glu Gln Pro Leu Leu Val Glu Glu Ile Gln Arg
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